<u>RAW SEQUENCE LISTING</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: ___ 10/567,876 ___

Source: ___ IF,WP ___

Date Processed by STIC: ___ 11/01/2006 ___

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 11/01/2006
PATENT APPLICATION: US/10/567,876   TIME: 14:42:01

Input Set : N:\Crf3\RULE60\10567876.RAW
Output Set: N:\CRF4\11012006\J567876.raw

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      1 <110> APPLICANT: Lovelace Respiratory Research Institute
      2        Tesfaigzi, Yohannes
      3        Belinsky, Steven A.
      4 <120> TITLE OF INVENTION: Metalloproteinase Gene Polymorphism in COPD
      5 <130> FILE REFERENCE: 41543-0302
C-->  6 <140> CURRENT APPLICATION NUMBER: US/10/567,876
      7 <141> CURRENT FILING DATE: 2006-02-08
      8 <150> PRIOR APPLICATION NUMBER: PCT/US04/26035
      9 <151> PRIOR FILING DATE: 2004-08-11
     10 <150> PRIOR APPLICATION NUMBER: US 60/494,631
     11 <151> PRIOR FILING DATE: 2003-08-11
     12 <160> NUMBER OF SEQ ID NOS: 17
     13 <170> SOFTWARE: PatentIn version 3.3
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     16 <211> LENGTH: 22
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     35 <212> TYPE: DNA
     36 <213> ORGANISM: Artificial
     37 <220> FEATURE:
     38 <223> OTHER INFORMATION: Synthetic sense primer for MMP-9 Gln279Arg SNP
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     46 <220> FEATURE:
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62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial
64 <220> FEATURE:
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94 <223> OTHER INFORMATION: Xaa is Gln in the common variant and Arg in the rare variant
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99                   20                  25                  30
100       Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
101                   35                  40                  45
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   103          50                  55                  60
   104      Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
   105      65                  70                  75                  80
   106      Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
   107                          85                  90                  95
   108      Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
   109                  100                  105                  110
   110      Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
   111              115                  120                  125
   112      Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
   113          130                  135                  140
   114      Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
   115      145                  150                  155                  160
   116      Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
   117                  165                  170                  175
   118      Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
   119                  180                  185                  190
   120      Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
   121                  195                  200                  205
   122      Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
   123          210                  215                  220
   124      Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
   125      225                  230                  235                  240
   126      Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
   127                  245                  250                  255
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   129                  260                  265                  270
W--> 130      Ser Glu Arg Leu Tyr Thr Xaa Asp Gly Asn Ala Asp Gly Lys Pro Cys
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   133          290                  295                  300
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   135      305                  310                  315                  320
   136      Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
   137                  325                  330                  335
   138      Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
   139                  340                  345                  350
   140      Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
   141              355                  360                  365
   142      Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
   143          370                  375                  380
   144      Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
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   146      His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
   147                  405                  410                  415
   148      Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
   149                  420                  425                  430
   150      Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
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Input Set : N:\Crf3\RULE60\10567876.RAW
Output Set: N:\CRF4\11012006\J567876.raw

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152       Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
153           450             455                 460
154       Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
155       465             470                 475             480
156       Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
157                   485             490                 495
158       Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
159               500             505                 510
160       Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly
161           515             520                 525
162       Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
163           530             535                 540
164       Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
165       545             550                 555             560
166       Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser
167                   565             570                 575
168       Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
169                   580             585                 590
170       Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
171               595             600                 605
172       Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
173           610             615                 620
174       Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
175       625             630                 635             640
176       Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
177                   645             650                 655
178       Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
179               660             665                 670
180       Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
181           675             680                 685
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184       Pro Glu Asp
185           705
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188 <211> LENGTH: 7639
189 <212> TYPE: DNA
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192 <221> NAME/KEY: misc_feature
193 <222> LOCATION: (2665)..(2665)
194 <223> OTHER INFORMATION: n is a in the common variant and g in the rare variant
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197     ctgcccccag acagcgccag tccacccttg tgctcttccc tggagacctg agaaccaatc     120
198     tcaccgacag gcagctggca gaggtgggca aacacctagt ctagagttgg ggagggctgt     180
199     ccgtgagggt gttgagtgtc ccagagagga tgcaggggcct cagaggagat gctttagggg     240
200     tgtgttggtg gtgatgggcg tatctgaaga acagaggtgt ccagggttag gcagtggggg     300
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      203   gggagtgaac aggggcaaac cttatgcagc tgtggggtag aaatgggcta gaggcatcca   480
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      209   cgcttgagtc caggaggtcc aggctgcagt gggctgatac cgtctctccg aaaaagaaaa   840
      210   agaaaaaaga ctccctccat gagtgtctgg agggagtcct ttggccccag ctgggcagag   900
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      212   atggttacac tcgggtggca gagatgcgtg gagagtcgaa atctctgggg cctgcgctgc  1020
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      214   aggccatgcg aaccccacgg tgcggggtcc cagacctggg cagattccaa acctttgagg  1140
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      216   cggggtgggg cggggaggcc aggtctggct cttgggccag cggtgaacat gtcctgtctt  1260
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/01/2006
PATENT APPLICATION: US/10/567,876   TIME: 14:42:02

Input Set : **N:\Crf3\RULE60\10567876.RAW**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 279
Seq#:10; N Pos. 2665
Seq#:11; N Pos. 841

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 94

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,12,13,14,15,16,17

VERIFICATION SUMMARY   DATE: 11/01/2006
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L:6 M:270 C: Current Application Number differs, Replaced Current Application Number
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:272
L:240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:2640
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:840